



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.5 [Nov-16-2002]

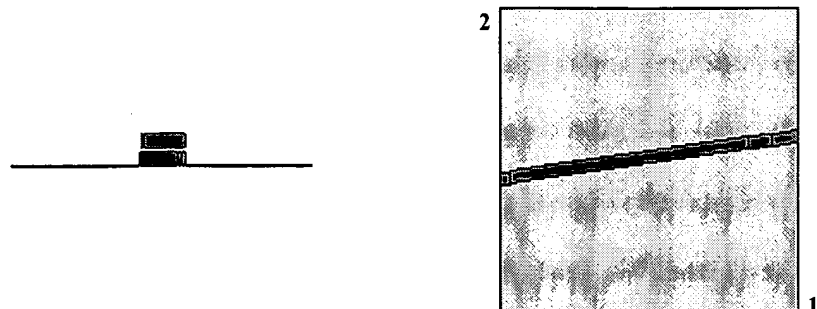
Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☒ Align

Sequence 1 gi\_1271750 yz97c02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290978 5' similar to PIR:S01302 S01302 hypothetical protein, 58K ;

Length 386 (1..386)

Sequence 2 gi\_16588686

Length 2677 (1..2677)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 694 bits (361), Expect = 0.0  
Identities = 383/387 (98%), Gaps = 3/387 (0%)  
Strand = Plus / Plus

```
Query: 1 tccaaagctgggaan-tctgtgttccggccatgaacgtcaatgattctgttaccaaacag 59
      1164 tccaaagctgggaagctctgtgttccggccatgaacgtcaatgattctgttaccaaacag 1223
Sbjct: 266 S K A G K L C V P A M N V N D S V T K Q

Query: 60 aagtttgataacttgactgctgcccagagaatccatgttgatggcctgaagaggaccaca 119
      1224 aagtttgataacttgactgctgcccagagaatccatgttgatggcctgaagaggaccaca 1283
Sbjct: 286 K F D N L Y C C R E S I L D G L K R T T

Query: 120 gatgtgatgtttggtgggaacaagtgggtggtgtgtggctatggtgaggtaggcaagggc 179
      1284 gatgtgatgtttggtgggaacaagtgggtggtgtgtggctatggtgaggtaggcaagggc 1343
Sbjct: 306 D V M F G G K Q V V V C G Y G E V G K G

Query: 180 tgctgtgctgctctcaaagctcttgaggcaattgtctacattaccgaaatcgaccccatc 239
      1344 tgctgtgctgctctcaaagctcttgaggcaattgtctacattaccgaaatcgaccccatc 1403
Sbjct: 326 C C A A L K A L G A I V Y I T E I D P I

Query: 240 tgtgctctgcaggcctgcatggatgggttcagggtggttaaagctaaatgaagtcacccg 299
      1404 tgtgctctgcaggcctgcatggatgggttcagggtggttaaagctaaatgaagtcacccg 1463
Sbjct: 346 C A L Q A C M D G F R V V K L N E V I R

Query: 300 caagtcgatgtcgtataaacttngcacaggaaataagaatgtagtgcacggngagcact 359
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Sbjct: 1464 caagtcgatgtcgtaataactt-gcacaggaaataagaatgtagtgacacgg-gagcact 1521  
S-adenosylhomocysteine hydrolas> 366 Q V D V V I T C T G N K N V V T R E H

Query: 360 tggatcgcatgaaaaacagttgtatcg 386  
|||||  
Sbjct: 1522 tggatcgcatgaaaaacagttgtatcg 1548  
S-adenosylhomocysteine hydrolas> 385 L D R M K N S C I

CPU time: 0.06 user secs. 0.05 sys. secs 0.11 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 6  
Number of Sequences: 0  
Number of extensions: 6  
Number of successful extensions: 4  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 386  
length of database: 8,484,804,551  
effective HSP length: 24  
effective length of query: 362  
effective length of database: 8,484,804,527  
effective search space: 3071499238774  
effective search space used: 3071499238774  
T: 0  
A: 0  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 20 (39.1 bits)